

MOLECULAR DIVERSITY AND PHENOTYPIC CHARACTERIZATION OF *SACCHAROMYCES SP.* STRAINS ISOLATED FROM THE VINHO VERDE WINE REGION

Schuller D., Alves H., Sampaio P., Pais C. and M. Casal*

Centro de Biologia, Universidade do Minho, Braga, Portugal;

* Corresponding author: mcasal@bio.uminho.pt

An extensive study was performed in order to better understand the biogeography and biodiversity of *Saccharomyces* sp. strains isolated from the enological fermentative microflora of the Vinho Verde Wine Region. The 930 isolates collected during 2001 and 2002 from 6 different sampling points and grape maturation stages in each of 3 vineyards (Baião, Ponte de Lima and Monção) of the Vinho Verde Region were assigned to 150 distinct genetic patterns based on mitochondrial DNA restriction fragment length polymorphisms (mtDNA RFLP). All 150 isolates were further analyzed in 6 microsatellite loci [1], and AMOVA analysis was performed using the program Arlequin [2]. A significant genetic variation between the genotypes originating from the 3 different vineyards was found, while no variation was found among the isolates of each of the 3 vineyards that were collected in different years, sampling points or grape maturation stages. In order to evaluate the oenological potential of the strain collection, 220 strains were screened for high ethanol tolerance, capacity to utilize acetic or malic acid and for low acetic acid and H₂S production. A remarkable heterogeneity of phenotypical biodiversity was found, and only 6 strains (2.7 %) of the 220 isolates showed the desired phenotypical traits.

[1] Pérez, M.A., Gallego, F.J., Martinez, I. and Hidalgo, P. 2001. Lett. Appl. Microbiol. 33, 461-466.

[2] Schneider, S., Kueffer, J-M., Roessli, D. and Excoffier, L. 1997. ARLEQUIN version 1.1. Software for population genetics data analysis. Geneva, Switzerland